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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/060,065

DATE: 07/18/2002

TIME: 13:19:18

Input Set : A:\06501-099002.txt

Output Set: N:\CRF3\07182002\J060065.raw

3 <110> APPLICANT: Toshio Ota  
 4 Takao Isogai  
 5 Tetsuo Nishikawa  
 6 Koji Hayashi  
 7 Kaoru Otsuka  
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 11 Ai Wakamatsu  
 12 Keiichi Nagai  
 13 Tetsuji Otsuki  
 14 Shin-Ichi Funahashi  
 15 Chiaki Senoo  
 16 Jun-Ichi Nezu  
 18 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE  
 20 <130> FILE REFERENCE: 06501-099002  
 22 <140> CURRENT APPLICATION NUMBER: US 10/060,065  
 23 <141> CURRENT FILING DATE: 2002-01-29  
 25 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05061  
 26 <151> PRIOR FILING DATE: 2000-07-28  
 28 <150> PRIOR APPLICATION NUMBER: US 60/159,590  
 29 <151> PRIOR FILING DATE: 1999-10-18  
 31 <150> PRIOR APPLICATION NUMBER: US 60/183,322  
 32 <151> PRIOR FILING DATE: 2000-02-17  
 34 <150> PRIOR APPLICATION NUMBER: JP 11-248036  
 35 <151> PRIOR FILING DATE: 1999-07-29  
 37 <150> PRIOR APPLICATION NUMBER: JP 2000-118776  
 38 <151> PRIOR FILING DATE: 2000-01-11  
 40 <150> PRIOR APPLICATION NUMBER: JP 2000-183767  
 41 <151> PRIOR FILING DATE: 2000-05-02  
 43 <150> PRIOR APPLICATION NUMBER: JP 2000-241899  
 44 <151> PRIOR FILING DATE: 2000-06-09  
 46 <160> NUMBER OF SEQ ID NOS: 43  
 48 <170> SOFTWARE: PatentIn Ver. 2.0  
 50 <210> SEQ ID NO: 1  
 51 <211> LENGTH: 2174  
 52 <212> TYPE: DNA  
 53 <213> ORGANISM: Homo sapiens  
 55 <220> FEATURE:  
 56 <221> NAME/KEY: CDS  
 57 <222> LOCATION: (366)..(1619)  
 59 <400> SEQUENCE: 1  
 60 cccgcgcttc tcgctgccca gccccgggga gggaggcggg gccgcgaccc cggcgcggggt 60

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61 ggggcgaatg cgttcccagc gggtagcctg gggctggtgc agagttccaa gcccacggcc 120
62 ccggtcgcgg cctcgccgcc ctcccgcgcc ccgcgcggg agcgggccta gagcgctcgc 180
63 ctgcccctc cgcgagcagg gctctggcgc ccgcccctgt ccgcaccgct ggcagcctga 240
64 agagagtcgc tggcgtggt cgccgctagg taggatatat ctgcattctg aaaggaagat 300
65 aaaacaaaag ccttcttttg aatagatgga tttttgtcac tttctgtgtg aactaaagtg 360
66 attca atg tct ctt ttg gat tgc ttc tgc act tca aga aca caa gtt gaa 410
67      Met Ser Leu Leu Asp Cys Phe Cys Thr Ser Arg Thr Gln Val Glu
68      1          5          10          15
70 tca ctc aga cct gaa aaa cag tct gaa acc agt atc cat caa tac ttg 458
71 Ser Leu Arg Pro Glu Lys Gln Ser Glu Thr Ser Ile His Gln Tyr Leu
72      20          25          30
74 gtt gat gag cca acc ctt tcc tgg tca cgt cca tcc act aga gcc agt 506
75 Val Asp Glu Pro Thr Leu Ser Trp Ser Arg Pro Ser Thr Arg Ala Ser
76      35          40          45
78 gaa gta cta tgt tcc acc aac gtt tct cac tat gag ctc caa gta gaa 554
79 Glu Val Leu Cys Ser Thr Asn Val Ser His Tyr Glu Leu Gln Val Glu
80      50          55          60
82 ata gga aga gga ttt gac aac ttg act tct gtc cat ctt gca cgg cat 602
83 Ile Gly Arg Gly Phe Asp Asn Leu Thr Ser Val His Leu Ala Arg His
84      65          70          75
86 act ccc aca gga aca ctg gta act ata aaa att aca aat ctg gaa aac 650
87 Thr Pro Thr Gly Thr Leu Val Thr Ile Lys Ile Thr Asn Leu Glu Asn
88 80          85          90          95
90 tgc aat gaa gaa cgc ctg aaa gct tta cag aaa gcc gtg att cta tcc 698
91 Cys Asn Glu Glu Arg Leu Lys Ala Leu Gln Lys Ala Val Ile Leu Ser
92      100          105          110
94 cac ttt ttc cgg cat ccc aat att aca act tat tgg aca gtt ttc act 746
95 His Phe Phe Arg His Pro Asn Ile Thr Thr Tyr Trp Thr Val Phe Thr
96      115          120          125
98 gtt ggc agc tgg ctt tgg gtt att tct cca ttt atg gcc tat ggt tca 794
99 Val Gly Ser Trp Leu Trp Val Ile Ser Pro Phe Met Ala Tyr Gly Ser
100     130          135          140
102 gca agt caa ctc ttg agg acc tat ttt cct gaa gga atg agt gaa act 842
103 Ala Ser Gln Leu Leu Arg Thr Tyr Phe Pro Glu Gly Met Ser Glu Thr
104     145          150          155
106 tta ata aga aac att ctc ttt gga gcc gtg aga ggg ttg aac tat ctg 890
107 Leu Ile Arg Asn Ile Leu Phe Gly Ala Val Arg Gly Leu Asn Tyr Leu
108 160          165          170          175
110 cac caa aat ggc tgt att cac agg agt att aaa gcc agc cat atc ctc 938
111 His Gln Asn Gly Cys Ile His Arg Ser Ile Lys Ala Ser His Ile Leu
112     180          185          190
114 att tct ggt gat ggc cta gtg acc ctc tct ggc ctg tcc cat ctg cat 986
115 Ile Ser Gly Asp Gly Leu Val Thr Leu Ser Gly Leu Ser His Leu His
116     195          200          205
118 agt ttg gtt aag cat gga cag agg cat agg gct gtg tat gat ttc cca 1034
119 Ser Leu Val Lys His Gly Gln Arg His Arg Ala Val Tyr Asp Phe Pro
120     210          215          220
122 cag ttc agc aca tca gtg cag ccg tgg ctg agt cca gaa cta ctg aga 1082
123 Gln Phe Ser Thr Ser Val Gln Pro Trp Leu Ser Pro Glu Leu Leu Arg

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124      225      230      235
126 cag gat tta cat ggg tat aat gtg aag tca gat att tac agt gtt ggg 1130
127 Gln Asp Leu His Gly Tyr Asn Val Lys Ser Asp Ile Tyr Ser Val Gly
128 240      245      250      255
130 att aca gca tgt gaa tta gcc agt ggg cag gtg cct ttc cag gac atg 1178
131 Ile Thr Ala Cys Glu Leu Ala Ser Gly Gln Val Pro Phe Gln Asp Met
132      260      265      270
134 cat aga act cag atg ctg tta cag aaa ctg aaa ggt cct cct tat agc 1226
135 His Arg Thr Gln Met Leu Leu Gln Lys Leu Lys Gly Pro Pro Tyr Ser
136      275      280      285
138 cca ttg gat atc agt att ttc cct caa tca gaa tcc aga atg aaa aat 1274
139 Pro Leu Asp Ile Ser Ile Phe Pro Gln Ser Glu Ser Arg Met Lys Asn
140      290      295      300
142 tcc cag tca ggt gta gac tct ggg att gga gaa agt gtg ctt gtc tcc 1322
143 Ser Gln Ser Gly Val Asp Ser Gly Ile Gly Glu Ser Val Leu Val Ser
144      305      310      315
146 agt gga act cac aca gta aat agt gac cga tta cac aca cca tcc tca 1370
147 Ser Gly Thr His Thr Val Asn Ser Asp Arg Leu His Thr Pro Ser Ser
148 320      325      330      335
150 aaa act ttc tct cct gcc ttc ttt agc ttg gta cag ctc tgt ttg caa 1418
151 Lys Thr Phe Ser Pro Ala Phe Phe Ser Leu Val Gln Leu Cys Leu Gln
152      340      345      350
154 caa gat cct gag aaa agg cca tca gca agc agt tta ttg tcc cat gtt 1466
155 Gln Asp Pro Glu Lys Arg Pro Ser Ala Ser Ser Leu Leu Ser His Val
156      355      360      365
158 ttc ttc aaa cag atg aaa gaa gaa agc cag gat tca ata ctt tca ctg 1514
159 Phe Phe Lys Gln Met Lys Glu Glu Ser Gln Asp Ser Ile Leu Ser Leu
160      370      375      380
162 ttg cct cct gct tat aac aag cca tca ata tca ttg cct cca gtg tta 1562
163 Leu Pro Pro Ala Tyr Asn Lys Pro Ser Ile Ser Leu Pro Pro Val Leu
164      385      390      395
166 cct tgg act gag cca gaa tgt gat ttt cct gat gaa aaa gac tca tac 1610
167 Pro Trp Thr Glu Pro Glu Cys Asp Phe Pro Asp Glu Lys Asp Ser Tyr
168 400      405      410      415
170 tgg gaa ttc tagggctgcc aaatcatttt atgtcctata tacttgacac 1659
171 Trp Glu Phe
173 tttctccttg ctgctttttc ttctgtatct ctaggtacaa ataccagaat tatacttgaa 1719
174 aatacagttg gtgcactgga gaatctatta tttaaaacca ctctgttcaa aggggcacca 1779
175 gtttgtagtc cctctgtttc gcacagagta ctatgacaag gaaacatcag aattactaat 1839
176 ctagctagtg tcaatttattc tggaattttt ttctaagctg tgactaactc tttttatctc 1899
177 tcaatataat ttttgagcca gtttaattttt ttcagtattt tgctgtccct tgggaatggg 1959
178 ccctcagagg acagtgttc caagtacatc ttctcccaga ttctctggcc tttttaatga 2019
179 gctattgtta aaccaacagg ctagttttatc ttacatcaga cccttttctg gtagagggaa 2079
180 aatgtttgtg ctttcccttt ttcttctgtt aatacttatg gtaacaccta actgagcctc 2139
181 actcacatta aatgattcac ttgaaatata tacag 2174
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 418
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens

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188 &lt;400&gt; SEQUENCE: 2

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189 Met Ser Leu Leu Asp Cys Phe Cys Thr Ser Arg Thr Gln Val Glu Ser
190 1 5 10 15
191 Leu Arg Pro Glu Lys Gln Ser Glu Thr Ser Ile His Gln Tyr Leu Val
192 20 25 30
193 Asp Glu Pro Thr Leu Ser Trp Ser Arg Pro Ser Thr Arg Ala Ser Glu
194 35 40 45
195 Val Leu Cys Ser Thr Asn Val Ser His Tyr Glu Leu Gln Val Glu Ile
196 50 55 60
197 Gly Arg Gly Phe Asp Asn Leu Thr Ser Val His Leu Ala Arg His Thr
198 65 70 75 80
199 Pro Thr Gly Thr Leu Val Thr Ile Lys Ile Thr Asn Leu Glu Asn Cys
200 85 90 95
201 Asn Glu Glu Arg Leu Lys Ala Leu Gln Lys Ala Val Ile Leu Ser His
202 100 105 110
203 Phe Phe Arg His Pro Asn Ile Thr Tyr Trp Thr Val Phe Thr Val
204 115 120 125
205 Gly Ser Trp Leu Trp Val Ile Ser Pro Phe Met Ala Tyr Gly Ser Ala
206 130 135 140
207 Ser Gln Leu Leu Arg Thr Tyr Phe Pro Glu Gly Met Ser Glu Thr Leu
208 145 150 155 160
209 Ile Arg Asn Ile Leu Phe Gly Ala Val Arg Gly Leu Asn Tyr Leu His
210 165 170 175
211 Gln Asn Gly Cys Ile His Arg Ser Ile Lys Ala Ser His Ile Leu Ile
212 180 185 190
213 Ser Gly Asp Gly Leu Val Thr Leu Ser Gly Leu Ser His Leu His Ser
214 195 200 205
215 Leu Val Lys His Gly Gln Arg His Arg Ala Val Tyr Asp Phe Pro Gln
216 210 215 220
217 Phe Ser Thr Ser Val Gln Pro Trp Leu Ser Pro Glu Leu Leu Arg Gln
218 225 230 235 240
219 Asp Leu His Gly Tyr Asn Val Lys Ser Asp Ile Tyr Ser Val Gly Ile
220 245 250 255
221 Thr Ala Cys Glu Leu Ala Ser Gly Gln Val Pro Phe Gln Asp Met His
222 260 265 270
223 Arg Thr Gln Met Leu Leu Gln Lys Leu Lys Gly Pro Pro Tyr Ser Pro
224 275 280 285
225 Leu Asp Ile Ser Ile Phe Pro Gln Ser Glu Ser Arg Met Lys Asn Ser
226 290 295 300
227 Gln Ser Gly Val Asp Ser Gly Ile Gly Glu Ser Val Leu Val Ser Ser
228 305 310 315 320
229 Gly Thr His Thr Val Asn Ser Asp Arg Leu His Thr Pro Ser Ser Lys
230 325 330 335
231 Thr Phe Ser Pro Ala Phe Phe Ser Leu Val Gln Leu Cys Leu Gln Gln
232 340 345 350
233 Asp Pro Glu Lys Arg Pro Ser Ala Ser Ser Leu Leu Ser His Val Phe
234 355 360 365
235 Phe Lys Gln Met Lys Glu Glu Ser Gln Asp Ser Ile Leu Ser Leu Leu
236 370 375 380

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237 Pro Pro Ala Tyr Asn Lys Pro Ser Ile Ser Leu Pro Pro Val Leu Pro
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240                      405                      410                      415
241 Glu Phe
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245 <211> LENGTH: 2718
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
249 <220> FEATURE:
250 <221> NAME/KEY: CDS
251 <222> LOCATION: (33)..(2627)
253 <400> SEQUENCE: 3
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256                      1                      5
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259 Ser Ser Asp Pro Ala Leu Ile Gly Leu Ser Thr Ser Val Ser Asp Ser
260                      10                      15                      20
262 aat ttt tcc tct gaa gag cct tca agg aaa aat ccc aca cgc tgg tca 149
263 Asn Phe Ser Ser Glu Glu Pro Ser Arg Lys Asn Pro Thr Arg Trp Ser
264                      25                      30                      35
266 aca aca gct ggc ttc ctc aag cag aac act gct ggg agt cct aaa gcc 197
267 Thr Thr Ala Gly Phe Leu Lys Gln Asn Thr Ala Gly Ser Pro Lys Ala
268 40                      45                      50                      55
270 tgc gac agg aag aaa gat gaa aac tac aga agc ctc ccg cgg gat act 245
271 Cys Asp Arg Lys Lys Asp Glu Asn Tyr Arg Ser Leu Pro Arg Asp Thr
272                      60                      65                      70
274 agt aac tgg tct aac caa ttt cag aga gac aat gct cgc tcg tct ctg 293
275 Ser Asn Trp Ser Asn Gln Phe Gln Arg Asp Asn Ala Arg Ser Ser Leu
276                      75                      80                      85
278 agt gcc agt cac cca atg gtg ggc aag tgg cag gag aaa caa gaa cag 341
279 Ser Ala Ser His Pro Met Val Gly Lys Trp Gln Glu Lys Gln Glu Gln
280                      90                      95                      100
282 gat gag gat ggg aca gaa gag gat aac agt cgt gtt gaa cct gtt gga 389
283 Asp Glu Asp Gly Thr Glu Glu Asp Asn Ser Arg Val Glu Pro Val Gly
284                      105                      110                      115
286 cat gct gac acg ggt ttg gag cat ata ccc aac ttt tct ctg gat gat 437
287 His Ala Asp Thr Gly Leu Glu His Ile Pro Asn Phe Ser Leu Asp Asp
288 120                      125                      130                      135
290 atg gta aag ctc gta gaa gtc ccc aac gat gga ggg cct ctg gga atc 485
291 Met Val Lys Leu Val Glu Val Pro Asn Asp Gly Gly Pro Leu Gly Ile
292                      140                      145                      150
294 cat gta gtg cct ttc agt gct cga ggc ggc aga acc ctg ggg tta tta 533
295 His Val Val Pro Phe Ser Ala Arg Gly Gly Arg Thr Leu Gly Leu Leu
296                      155                      160                      165
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300                      170                      175                      180

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VERIFICATION SUMMARY

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